



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Laus, Reiner  
Ruegg, Curtis L.  
Shapero, Michael H.  
Yang, Demao
- (ii) TITLE OF INVENTION: Composition and Method for  
Producing an Immune Response Against Tumor-Related Antigens

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Iota Pi Law Group
- (B) STREET: P.O. Box 60850
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: US
- (F) ZIP: 94306

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/402,845
- (B) FILING DATE: 10-APR-1998
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/043,301
- (B) FILING DATE: 11-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Dehlinger, Peter J.
- (B) REGISTRATION NUMBER: 28,006
- (C) REFERENCE/DOCKET NUMBER: 7636-0013.10

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650-324-0880
- (B) TELEFAX: 650-324-0960

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: mouse prostatic acid phosphatase (mPAP)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGGAGCCG	TTCCTCTGCC	CCTGAGCCCG	ACAGCAAGCC	TCAGCCTTGG	CTTCTTGCTC	60
CTGCTTTTCTC	TCTGCCTGGA	CCCAGGCCAA	GCCAAGGAGT	TGAAGTTTGT	GACATTGGTG	120
TTTCGACATG	GAGACCGAGG	TCCCATCGAG	ACCTTTCCTA	CCGACCCCAT	TACGGAATCC	180
TCGTGGCCAC	AAGGATTTGG	CCAACCTACC	CAGTGGGGCA	TGGAACAGCA	CTACGAACCTT	240
GGAAGTTATA	TAAGGAAAAG	ATACGGAAGA	TTCTTGAACG	ACACCTATAA	GCATGATCAG	300
ATTTATATCC	GGAGCACAGA	TGTGGACAGG	ACTTTGATGA	GTGCTATGAC	AAACCTTGCA	360
GCCCTGTTTC	CTCCAGAGGG	GATCAGCATC	TGGAATCCTA	GACTGCTCTG	GCAGCCCATC	420
CCAGTGCACA	CCGTGTCTCT	CTCTGAGGAT	CGGTTGCTGT	ACCTGCCTTT	CAGAGACTGC	480
CCTCGTTTTG	AAGAACTCAA	GAGTGAGACT	TTAGAATCTG	AGGAATTCTT	GAAGAGGCTT	540
CATCCATATA	AAAGCTTCCT	GGACACCTTG	TCGTCGCTGT	CGGGATTCTGA	TGACCAGGAT	600
CTTTTTTGGA	TCTGGAGTAA	AGTTTATGAC	CCTTTATTCT	GCGAGAGTGT	TCACAATTTT	660
ACCTTGCCCT	CCTGGGCCAC	CGAGGACGCC	ATGATTAAGT	TGAAAGAGCT	ATCAGAATTA	720
TCTCTGCTAT	CACCTTTATG	AATTCACAAG	CAGAAAGAGA	AATCTCGACT	CCAAGGGGGC	780
GTCCTGGTCA	ATGAAATCCT	CAAGAATATG	AAGCTTGCAA	CTCAGCCACA	GAAGTATAAA	840
AAGCTGGTCA	TGTATTCCGC	ACACGACACT	ACCGTGAGTG	GCCTGCAGAT	GGCGCTAGAT	900
GTTTATAATG	GAGTTCTGCC	TCCCTACGCT	TCTTGCCACA	TGATGGAATT	GTACCATGAT	960
AAGGGGGGGC	ACTTTGTGGA	GATGTACTAT	CGGAATGAGA	CCCAGAACGA	GCCCTACCCA	1020
CTCACGCTGC	CAGGCTGCAC	CCACAGCTGC	CCTCTGGAGA	AGTTTGCGGA	GCTACTGGAC	1080
CCGGTGATCC	CBCAGGACTG	GGCCACGGAG	TGTATGGCCA	CAAGCAGCCA	CCAAGGTACT	1140
GTGGGCGCTT	TGGGTTAG					1158

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: mouse prostatic acid phosphatase (mPAP) coding sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Ala	Val	Pro	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Ser	Leu	Ser	Leu
1				5				10					15		
Gly	Phe	Leu	Leu	Leu	Leu	Ser	Leu	Cys	Leu	Asp	Pro	Gly	Gln	Ala	Lys
		20						25					30		
Glu	Leu	Lys	Phe	Val	Thr	Leu	Val	Phe	Arg	His	Gly	Asp	Arg	Gly	Pro
		35					40					45			
Ile	Glu	Thr	Phe	Pro	Thr	Asp	Pro	Ile	Thr	Glu	Ser	Trp	Pro	Gln	
	50					55				60					
Gly	Phe	Gly	Gln	Leu	Thr	Gln	Trp	Gly	Met	Glu	Gln	His	Tyr	Glu	Leu
65					70				75					80	
Gly	Ser	Tyr	Ile	Arg	Lys	Arg	Tyr	Gly	Arg	Phe	Leu	Asn	Asp	Thr	Tyr
			85					90					95		
Lys	His	Asp	Gln	Ile	Tyr	Ile	Arg	Ser	Thr	Asp	Val	Asp	Arg	Thr	Leu
			100					105					110		
Met	Ser	Ala	Met	Thr	Asn	Leu	Ala	Leu	Phe	Pro	Pro	Glu	Gly	Ile	
	115					120						125			
Ser	Ile	Trp	Asn	Pro	Arg	Leu	Leu	Trp	Gln	Pro	Ile	Pro	Val	His	Thr
	130					135					140				
Val	Ser	Leu	Ser	Glu	Asp	Arg	Leu	Leu	Tyr	Leu	Pro	Phe	Arg	Asp	Cys
145				150					155					160	
Pro	Arg	Phe	Glu	Glu	Leu	Lys	Ser	Glu	Thr	Leu	Glu	Ser	Glu	Glu	Phe
			165					170					175		
Leu	Lys	Arg	Leu	His	Pro	Tyr	Lys	Ser	Phe	Leu	Asp	Thr	Leu	Ser	Ser
			180				185						190		
Leu	Ser	Gly	Phe	Asp	Asp	Gln	Asp	Leu	Phe	Gly	Ile	Trp	Ser	Lys	Val
	195					200						205			
Tyr	Asp	Pro	Leu	Phe	Cys	Glu	Ser	Val	His	Asn	Phe	Thr	Leu	Pro	Ser
	210					215						220			

Trp Ala Thr Glu Asp Ala Met Ile Lys Leu Lys Glu Leu Ser Glu Leu  
 225 230 235 240  
 Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser Arg  
 245 250 255  
 Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Lys Asn Met Lys Leu  
 260 265 270  
 Ala Thr Gln Pro Gln Lys Tyr Lys Lys Leu Val Met Tyr Ser Ala His  
 275 280 285  
 Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn Gly  
 290 295 300  
 Val Leu Pro Pro Tyr Ala Ser Cys His Met Met Glu Leu Tyr His Asp  
 305 310 315 320  
 Lys Gly Gly His Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln Asn  
 325 330 335  
 Glu Pro Tyr Pro Leu Thr Leu Pro Gly Cys Thr His Ser Cys Pro Leu  
 340 345 350  
 Glu Lys Phe Ala Glu Leu Leu Asp Pro Val Ile Pro Gln Asp Trp Ala  
 355 360 365  
 Thr Glu Cys Met Ala Thr Ser Ser His Gln Gly Thr Val Gly Ala Leu  
 370 375 380  
 Gly  
 385

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: gene specific primer for 5' end cloning of mPAP from mouse prostate (first round)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATTCCGGTA GTACATCTCC AC

22

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: gene specific primer for 5' end cloning of mPAP from mouse prostate (second round)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCACAAACT TCAACTCCTT GG

22

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: gene specific primer for 3' end cloning  
of mPAP from mouse prostate (first round)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATGTACTAC CGGAATGAGA C

21

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: gene specific primer for 3' end cloning  
of mPAP from mouse prostate (second round)

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1, 10

(D) OTHER INFORMATION: \note: "where N is A, G, C, or T"

(A) NAME/KEY: Other

(B) LOCATION: 13

(D) OTHER INFORMATION: \note: "where R is A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

NGTGATCCCN CARGACTGG

19

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: synthetic anchor primer one (AP1) for  
mPAP cloning

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: synthetic anchor primer two (AP2) for  
mPAP cloning

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: forward primer (A31091) for mPAP amplification

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGTGCAGCA CTCCTAAGG

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: reverse primer (A31093) for mPAP amplification

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCACCTTCCTG CTGAGCTCC

19

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: signal peptide of the deduced amino acid sequence for mPAP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Ala Val Pro Leu Pro Leu Ser Pro Thr Ala Ser Leu Ser Leu  
1                      5                      10                      15  
Gly Phe Leu Leu Leu Leu Ser Leu Cys Leu Asp Pro Gly Gln Ala  
20                      25                      30